

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 10:03:04 : Search time 27.2727 Seconds
(without alignments)
4034.242 Million cell updates/sec

Title: US-09-125-005-6
Perfect score: 3384

Sequence: 1 MAQSTATSPDGGTTFEHLWS.....PDKARKQPIKEEFTAEIHH 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3014.5	89.1	631	11	Q9JJP2	Q9JJP2 mus musculus
2	2830.5	83.6	590	11	Q9JJP1	Q9JJP1 mus musculus
3	2507.5	74.1	514	11	Q9CU77	Q9CU77 mus musculus
4	2414.5	71.4	641	13	Q9W664	Q9W664 barbus barb
5	2379	70.3	497	11	Q9WUJ0	Q9WUJ0 mus musculus
6	1790	52.9	641	4	Q9UP28	Q9UP28 homo sapien
7	1790	52.9	680	4	Q9H3D4	Q9H3D4 homo sapien
8	1789	52.9	663	11	Q99JE3	Q99JE3 rattus norv
9	1789	52.9	680	11	Q88898	Q88898 mus musculus
10	1789	52.9	680	11	Q9JJP6	Q9JJP6 rattus norv
11	1786	52.8	641	4	O75195	O75195 homo sapien
12	1782	52.7	680	4	Q9UE10	Q9UE10 homo sapien
13	1743	51.5	586	11	O89097	O89097 mus musculus
14	1741	51.4	586	4	Q9UBV9	Q9UBV9 homo sapien
15	1740	51.4	586	11	Q99JE2	Q99JE2 rattus norv
16	1737	51.3	586	4	Q9P1B4	Q9P1B4 homo sapien

17	1727	51.0	586	4	O75080	O75080 homo sapien
18	1698.5	50.2	582	13	Q9DEC7	Q9DEC7 gallus gall
19	1470.5	43.5	501	4	Q9H3P8	Q9H3P8 homo sapien
20	1464.5	43.3	516	4	Q9P1B7	Q9P1B7 homo sapien
21	1464.5	43.3	516	4	Q9UP27	Q9UP27 homo sapien
22	1464.5	43.3	555	4	Q9H3D3	Q9H3D3 homo sapien
23	1459.5	43.1	538	11	Q99JD7	Q99JD7 rattus norv
24	1459.5	43.1	555	11	Q9QWZ0	Q9QWZ0 mus musculus
25	1459.5	43.1	555	11	Q99JD8	Q99JD8 rattus norv
26	1415.5	41.8	461	4	Q9P1B5	Q9P1B5 homo sapien
27	1415.5	41.8	461	4	Q9UP26	Q9UP26 homo sapien
28	1413.5	41.8	461	11	Q9QWY9	Q9QWY9 mus musculus
29	1410.5	41.7	461	11	Q99JD6	Q99JD6 rattus norv
30	1385	40.9	471	4	Q9NPH7	Q9NPH7 homo sapien
31	1336	39.5	416	4	Q9P1B6	Q9P1B6 homo sapien
32	1335.5	39.5	286	11	Q9D6A3	Q9D6A3 mus musculus
33	1302.5	38.5	470	11	Q99JE1	Q99JE1 rattus norv
34	1302.5	38.5	487	11	Q99JE0	Q99JE0 rattus norv
35	1297.5	38.3	448	4	O76078	O76078 homo sapien
36	1297.5	38.3	487	4	Q9H3D2	Q9H3D2 homo sapien
37	1284.5	38.0	483	11	O88897	O88897 mus musculus
38	1253.5	37.0	393	11	Q99JD9	Q99JD9 rattus norv
39	1248.5	36.9	393	4	O75922	O75922 homo sapien
40	1240.5	36.7	356	4	Q9OP74	Q9OP74 homo sapien
41	1238.5	36.6	389	11	O88899	O88899 mus musculus
42	1237.5	36.5	365	13	Q98SW0	Q98SW0 xenopus lae
43	994	29.4	232	4	Q96KRO	Q96KRO homo sapien
44	905.5	26.8	621	5	Q9NGC7	Q9NGC7 mya arenari
45	859.5	25.4	564	5	Q27937	Q27937 loligo forb

ALIGNMENTS

RESULT 1

Q9JJP2 PRELIMINARY; PRT; 631 AA.
AC Q9JJP2
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE P73 ALPHA PROTEIN.
GN TRP73 OR P73
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20179195; PubMed=10716451;
RA Yang A., Walker N., Bronson R., Raghad M., Oosterweel M., Bonnin J.,
Vagner C., Bonnet H., Dikkes P., Sharpe A., Mckee F., Caput D.;
RT p73-deficient mice have neurological, phenomonal and inflammatory
defects but lack spontaneous tumors.
RL Nature 404:99-103(2000).
DR EMBL; Y19234; CAB81953.1;
DR HSSP; O15350; 1COK.
DR MGD; MGI:1336991; Trp73
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 631 AA; 69095 MW; E364D566A90CBF1D CRC64;

Query Match 89.1%; Score 3014.5; DB 11; Length 631;
Best Local Similarity 88.8%; Pred. No. 3.6e-241;
Matches 569; Conservative 25; Mismatches 32; Indels 15; Gaps 6;

QY 1 MAQSTATSPDGGTTFEHLWSLEPDSTYFDLPQSSRGNEVGGTSSMDVFLHLEGMTTS 60

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Db 1 MAQ-----TSSSSSTFEHLWSLSDSYFDLPQPSQGTSEASGESENNMDVFLQG---- 53
QY 61 VMAQFNLLSSTMDQSSRAASAPYTPTEHAASVPTHTSPYAQPSSTEDTMSAPVIPSNTD 120
Db 54 -MAQFNLLSSAMDQSSRAAPSPYTPTEHAASAPHTSPYAQPSSTEDTMSAPVIPSNTD 112
QY 121 YGPHHFEVTFQOSTAKSATWTYSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180
Db 113 YGPHHFEVTFQOSTAKSATWTYSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 172
QY 181 YKKAHVTDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLLSQYVDDPVTGRQSVVVPY 240
Db 173 YKKAHVTDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLLSQYVDDPVTGRQSVVVPY 232
QY 241 EPPQVGTFTILYNFACNSCVGGMNRRPILIIITLEMRDQGVLGRRSFEGRICACPCR 300
Db 233 EPPQVGTFTILYNFACNSCVGGMNRRPILIIITLEMRDQGVLGRRSFEGRICACPCR 292
QY 301 DRKADEHYREQQALNESSAKNGAASKRAFQSPPAVPALGAGVKKRRHGDDETYLQVR 360
Db 293 DRKADEHYREQQALNESSAKNGAASKRAFQSPPAVPALGAGVKKRRHGDDETYLQVR 352
QY 361 GRENEFILLMKLESLELMELVPOPLVDYSR--QQQLLQRPSPHLPSPVSPMKNVH 418
Db 353 GRENEFILLMKLESLELMELVPOPLVDYSR--QQQLLQRPSPHLPSPVSPMKNVH 412
QY 419 GGKMLPSVNLQVQPPPHSSAAATPNLGPVPGMLNHHGAVPANGEMSSSHSAQSVSG 478
Db 413 GGKMLPSVNLQVQPPPHSSAAATPNLGPVPGMLNHHGAVPANGEMSSSHSAQSVSG 472
QY 479 SHCTPPPYHADPSLVSLFTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYR 538
Db 473 SHCTPPPYHADPSLVSLFTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYR 532
QY 539 MTIWGLQDLKQGHDXSTAQQLLR--SSNAATISIGSGELQORVMEAVHFRVHTITIP 597
Db 533 MTIWGLQDLKQGHDXSTAQQLLR--SSNAATISIGSGELQORVMEAVHFRVHTITIP 590
QY 598 NRGPGG--GPDEWADFGDLPDCKARKQPIKEEFTAEI 636
Db 591 NRGPGG--GPDEWADFGDLPDCKARKQPIKEEFTAEI 631

RESULT 2
Q9CU77 ID Q9CU77 PRELIMINARY; PRT; 590 AA.
AC Q9CU77;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE P73 DELTA-N PROTEIN.
GN TRP73 OR P73.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20179195; PubMed=10716451;
RA Yang A., Walker N., Bronson R., Kaghad M., Osterweil M., Bonnin J.,
RA Wagner C., Bonnet H., Dikkes P., Sharpe A., McKeon F., Caput D.;
RT "p73-deficient mice have neurological, phecomonal and inflammatory
RL defects but lack spontaneous tumors.";
RL Nature 404:99-103(2000).
RX EMBL; Y19235; CAB81954.1;
DR HSP; O15350; ICKO
DR MGD; MGI:1336991; Trp73.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
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DR ProDom; PD002681; P53; 1.
DR SMART; SMO0454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 590 AA; 64725 MW; 8580C7BFA21B5797 CRC64;

Query Match 83.68; Score 2830.5; DB 11; Length 590;
Best Local Similarity 91.7%; Pred. No. 5.8e-226;
Matches 531; Conservative 19; Mismatches 22; Indels 7; Gaps 4;

QY 63 AQFNLLSSTMDQSSRAASAPYTPTEHAASVPTHTSPYAQPSSTEDTMSAPVIPSNTDYP 122
Db 14 AQFNLLSSAMDQSSRAAPSPYTPTEHAASAPHTSPYAQPSSTEDTMSAPVIPSNTDYP 73
QY 123 GHHEFEVTFQOSTAKSATWTYSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 182
Db 74 GHHEFEVTFQOSTAKSATWTYSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 133
QY 183 KAHEVTDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLLSQYVDDPVTGRQSVVVPY 242
Db 134 KAHEVTDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLLSQYVDDPVTGRQSVVVPY 193
QY 243 PQVGTFTILYNFACNSCVGGMNRRPILIIITLEMRDQGVLGRRSFEGRICACPCR 302
Db 194 PQVGTFTILYNFACNSCVGGMNRRPILIIITLEMRDQGVLGRRSFEGRICACPCR 253
QY 303 KADEHYREQQALNESSAKNGAASKRAFQSPPAVPALGAGVKKRRHGDDETYLQVR 362
Db 254 KADEHYREQQALNESSAKNGAASKRAFQSPPAVPALGAGVKKRRHGDDETYLQVR 313
QY 363 ENFEILLMKLESLELMELVPOPLVDYSR--QQQLLQRPSPHLPSPVSPMKNVH 420
Db 314 ENFEILLMKLESLELMELVPOPLVDYSR--QQQLLQRPSPHLPSPVSPMKNVH 373
QY 421 MKLPSVNLQVQPPPHSSAAATPNLGPVPGMLNHHGAVPANGEMSSSHSAQSVSG 480
Db 374 VNKLSVNLQVQPPPHSSAAATPNLGPVPGMLNHHGAVPANGEMSSSHSAQSVSG 433
QY 481 CTPPPPYHADPSLVSLFTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYR 540
Db 434 CTPPPPYHADPSLVSLFTGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLGALKIPEQYR 493
QY 541 IWRGLQDLKQGHDXSTAQQLLR--SSNAATISIGSGELQORVMEAVHFRVHTITIP 599
Db 494 IWRGLQDLKQGHDXSTAQQLLR--SSNAATISIGSGELQORVMEAVHFRVHTITIP 551
QY 600 GPGG--GPDEWADFGDLPDCKARKQPIKEEFTAEI 636
Db 552 GGAGAVTGPDEWADFGDLPDCKARKQPIKEEFTAEI 590

RESULT 3
Q9CU77 ID Q9CU77 PRELIMINARY; PRT; 514 AA.
AC Q9CU77;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE TRANSFORMATION RELATED PROTEIN 73 (FRAGMENT).
GN TRP73...
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schramm L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL EMBL; AK017412; BAB30732.1;
 DR HSSP; O15350; ICOK.
 DR MGD; MGI:1336991; Ttp73.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00386; P53SUPPRESSOR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 514 AA; 56677 MW; 539AE64527CBF552 CRC64;

Query Match 74.1%; Score 2507.5; DB 11; Length 514;
 Best Local Similarity 91.5%; Pred. No. 2.8e-199;
 Matches 471; Conservative 19; Mismatches 18; Indels 7; Gaps 4;

QY 127 FEVTFQSSSTAKSATWYSPLLAKLYCQIAKTCPIQIKVSTPPPTAIRAMPVYKKAH 186
 DB 2 FEVTFQSSSTAKSATWYSPLLAKLYCQIAKTCPIQIKVSTPPPTAIRAMPVYKKAH 61
 QY 187 VTDVVKPCNHELGRDNFEGOSAPASHLRVNEGNNLSQYVDDPVTGROSVVYVPEPQVG 246
 DB 62 VTDVVKPCNHELGRDNFEGOSAPASHLRVNEGNNLSQYVDDPVTGROSVVYVPEPQVG 121
 QY 247 TEFTILYFNMCSSCVGGNNRRPILITILEMRDQVLRSGFGRICACGRDRKDE 306
 DB 122 TEFTILYFNMCSSCVGGNNRRPILITILEMRDQVLRSGFGRICACGRDRKDE 181
 QY 307 DHYREQQALNESSAKGAASKRAFQSPAPALGAGVKKRRHGDEDTYILQVRGRENFE 366
 DB 182 DHYREQQALNESSAKGAASKRAFQSPAPALGAGVKKRRHGDEDTYILQVRGRENFE 241
 QY 367 ILMKLSLELMELVLPQPLVDSYR--QQOQLLRPSHLOPPSYGVPVLPNKKVHGGMKL 424
 DB 242 ILMKLSLELMELVLPQPLVDSYR--QQOQLLRPSHLOPPSYGVPVLPNKKVHGGMKL 301
 QY 425 PVSNOVGQPPPHSSAATPNLGPVPGMLNHHGHPANGEMSSSSHAQSVYSGSHCTPP 484
 DB 302 PVSNOVGQPPPHSSAATPNLGPVPGMLNHHGHPANGEMSSSSHAQSVYSGSHCTPP 361
 QY 485 PPYHADPSLVFLGLGCPNCIEFTSQGLQSIYHLQNTIEDLGALKIPDYRTIWRG 544
 DB 362 PPYHADPSLVFLGLGCPNCIEFTSQGLQSIYHLQNTIEDLGALKIPDYRTIWRG 421
 QY 545 LQDLKQGHYDSTAQQLLR--SSNAATISIGSGELQVRVMEVHFFVRITITIPNRGGP 603
 DB 422 LQDLKQGHYDSTAQQLLR--SSNAATISIGSGELQVRVMEVHFFVRITITIPNRGGP 479
 QY 604 G--GPDEWADFGDLPCKARKQPIKEEFTAEI 636
 DB 480 AVTGPDEWADFGDLPCKARKQPIKEEFTAEI 514

RESULT 4

Q9W664
 ID Q9W664
 AC Q9W664;

PRELIMINARY; PRT; 641 AA.

DT 01-NOV-1999 (TREMELREL.12, Created)
 DT 01-NOV-1999 (TREMELREL.12, Last sequence update)
 DT 01-DEC-2001 (TREMELREL.19, Last annotation update)
 DE P73.
 OS Barbus barbus (Barbel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Barbus.
 OX NCBI_TaxID=40830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20362516; PubMed=10825664;
 RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
 RT "Molecular characterization of the first non-mammalian p73 cDNA.";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 126:49-57(2000).
 DR EMBL; AF043641; AAD27752.1;
 DR HSSP; O15350; ICOK.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00386; P53SUPPRESSOR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 SQ SEQUENCE 641 AA; 71090 MW; 4A215B21AEB16E4D CRC64;

Query Match 71.4%; Score 2414.5; DB 13; Length 641;
 Best Local Similarity 70.7%; Pred. No. 1.9e-191;
 Matches 456; Conservative 81; Mismatches 91; Indels 17; Gaps 8;

QY 4 STATSPDGGTTFEHLWSSLEPDSPTFDLPQSSRGNNVVGTT-----DSSMDVHF---L 54
 DB 2 SQSSPADGTTTFEHLWSTLEPDSPTFELPOAGHSGRGRVASSSLPSNRAEVCMDVHMMD 61
 QY 55 EGMTTSVMAQNLSSLMQDQ--MSRAASAPYTPHAASVTPHSPVAPSPSTFDMSPAP 113
 DB 62 RMDNVMVQSLLSSNEQGLGNRAASTPSYSETTSNVTPTSPSPQNSTFEMSPAP 121
 QY 114 VPSNTDYPGPHFEVTFQSSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPT 173
 DB 122 AIPSTNDYPGPHFEVTFQSSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPT 181
 QY 174 ATRAMPYTKAEHTVDVVKPCNHELGRDNFEGOSAPASHLRVNEGNNLSQYVDDPVTGR 233
 DB 182 VIRAMPYTKAEHTVDVVKPCNHELGRDNFEGOSAPASHLRVNEGNNLSQYVDDPVTGR 241
 QY 234 QSVVYVPEPQVPGTFTILYFNMCSSCVGGNNRRPILITILEMRDQVLRSGFGR 293
 DB 242 QSVVYVPEPQVPGTFTILYFNMCSSCVGGNNRRPILITILEMRDQVLRSGFGR 301
 QY 294 ICACGRDRKDEHYREQQALNESSAKGAASKRAFQSPAPALGAGVKKRRHGDE 353
 DB 302 ICACGRDRKDEHYREQQALNESSAKGAASKRAFQSPAPALGAGVKKRRHGDE 361
 QY 354 TYILOVRGRENFEILMKLSLELMELVLPQPLVDSYR--QQOQLLRPSHLOPPSYGVPVLS 412
 DB 362 MYIYVPGRENFDILMKLSLELMELVLPQPLVDSYR--QQOQLLRPSHLOPPSYGVPVLS 421
 QY 413 PMNKVHGGMKLPSVNLVQGPVPPHSSAATPNLGPVPGMLNHHGHPANGEMSSSSHA 472
 DB 422 NMNKHGSIKSLPSVNLVQGPVPPHSSAATPNLGPVPGMLNHHGHPANGEMSSSSHA 479
 QY 473 QSMVSGSHCTPPPPYHADPSLVFLGLGCPNCIEFTSQGLQSIYHLQNTIEDLGALK 532
 DB 480 QSLVSTSHCTPPPPYHADPSLVFLGLGCPNCIEFTSQGLQSIYHLQNTIEDLGALK 539
 QY 533 IPEQYRMTIWRGLQDLKQGHYDSTAQQLLR--SSNAATISIGSGELQVRVMEVHFFVR 591
 DB 540 IPEQYRMTIWRGLQDLKQGHYDSTAQQLLR--SSNAATISIGSGELQVRVMEVHFFVR 597
 QY 592 HTTIPNRGGPGGDEWADFGDLPCKARKQPIKEEFTAEI 636
 DB 598 HTTIPNRGGPGGDEWADFGDLPCKARKQPIKEEFTAEI 641

RESULT 5

Q9WUJ0 PRELIMINARY; PRT; 497 AA;
 ID Q9WUJ0; AC Q9WUJ0; DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
 DE F73 (FRAGMENT).
 GN TRP73.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D3 (129SV);
 RX MEDLINE=99247549; PubMed=10232589;
 RA Herranz M., Santos J., Salido E., Fernandez-Piqueras J., Serrano M.;
 RT "Mouse p73 gene maps to the distal part of chromosome 4 and might be
 RT involved in the progression of gamma-radiation-induced T-cell
 RT lymphomas";
 RL Cancer Res. 59:2068-2071(1999).
 DR EMBL; AF138873; AAC22113.1; -;
 DR HSP; O15350; ICOK.
 DR MGD; MGI:1336991; Trp73.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 FT NON_TER 1
 SQ SEQUENCE 497 AA; 54717 MW; 810C584F7D466025 CRC64;

Query Match 70.3%; Score 2379; DB 11; Length 497;
 Best Local Similarity 90.28; Pred. No. 1.2e-188;
 Matches 450; Conservative 19; Mismatches 22; Indels 8; Gaps 5;
 QY 144 YSPLKLLKVCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDF 203
 Db 1 YSPLKLLKVCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDF 60
 QY 204 NEGOSAPASHLRVSGNLSQYDDPVTGROSVVVYEPPOVGTEFTILYNFMCNNSCV 263
 Db 61 NEGOSAPASHLRVSGNLSQYDDPVTGROSVVVYEPPOVGTEFTILYNFMCNNSCV 120
 QY 264 GGNRRPILIIITLMDRGQVLGRSFEGRICACPGDRKADEHYREQQALNESSAKNG 323
 Db 121 GGNRRPILIIITLMDRGQVLGRSFEGRICACPGDRKADEHYREQQALNESSAKNG 180
 QY 324 ASKRAFKOSPAPVAPALGNGYKRRHGDEDPYIYQV-RGRNFEILMKLESLELMELVP 382
 Db 181 ASKRAFKOSPAPVAPALGNGYKRRHGDEDPYIYQV-RGRNFEILMKLESLELMELVP 240
 QY 383 QPLVDSYR--OQQLLRPSHLQPPSYGVLSPMNKYGKGNKLPVSNQVLVGQPPHSSA 440
 Db 241 QPLVDSYR--OQQLLRPSHLQPPSYGVLSPMNKYGKGNKLPVSNQVLVGQPPHSSA 300
 QY 441 ATPNLGPVPGMLNHNHGAHPANGEMSSSSAQSWSGSHCTPPPHADPSVSLTGL 500
 Db 301 AGPNLGPMSGMLNHNHGAHPANGEMSSSSAQSWSGSHCTPPPHADPSVSLTGL 360
 QY 501 GCPNCEYFTSGLOSIYHLQNLTTEDLGALKIPEQVMTWRLQDLKQGHSDYSTAQOL 560
 Db 361 GCPNCEYFTSGLOSIYHLQNLTTEDLGALKIPEQVMTWRLQDLKQGHSD--CCQOL 418
 QY 561 LR--SSNAATISGGSEIQRQRYEAVHFRVHTITIPNRRGGPG--GPDENADFGDLP 617
 Db 419 LRSSNAATISGGSEIQRQRYEAVHFRVHTITIPNRRGGAGVTPGPDENADFGDLP 478

QY 618 DCKARKQPIKEEFTAEIHH 636

Db 479 DCKSRKQPIKEEFTETESH 497

RESULT 6

Q9UP28 PRELIMINARY; PRT; 641 AA.
 ID Q9UP28; AC Q9UP28; DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE TA P63 ALPHA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities";
 RL Mol. Cell 2:305-316(1998).
 DR EMBL; AF075430; AAC62635.1; -;
 DR HSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 SQ SEQUENCE 641 AA; 72049 MW; 23A2E5EBAE63F605 CRC64;
 Query Match 52.9%; Score 1790; DB 4; Length 641;
 Best Local Similarity 55.18; Pred. No. 1.1e-139;
 Matches 366; Conservative 94; Mismatches 144; Indels 60; Gaps 18;
 QY 1 MAOSTAT---SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNEVVGTDSS 48
 Db 1 MSOSTOTNEFLSPE---VFQIHWDFLEQICVQPIDLNEVDFESEDGATNKI----EIS 53
 QY 49 MDVFEHLEGMTS-----VMAQFNLLSSTMDQMSKRAASASPYTPEHAA-SVPHSPYAP 102
 Db 54 MDQIRQDSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSYPAP 113
 QY 103 SSTFDMSAPVIPSNTDYPGPHHEVTFQSSSTAKSATWTYSPLKLLKCYIAKTCPIQ 162
 Db 114 SSTFDALSPAPISNTDYPGPHSFDVFSQSSSTAKSATWTYSPLKLLKCYIAKTCPIQ 173
 QY 163 IKYSTPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDFNEGOSAPASHLRVSGNLS 222
 Db 174 IKVTPPGGAVIRAMPYKKAHVTEVVKRCPNHELGRDFNEGOSAPASHLRVSGNLS 233
 QY 223 SQYVDPVTVTGRSVVYVPEPPQVGTEFTILYNFMCNNSCVGGMNRRPILIIITLMDRG 282
 Db 234 AQVDEPIATGROSLVLPVPEPPQVGTEFTILYNFMCNNSCVGGMNRRPILIIITLMDRG 293
 QY 283 QVLGRSFEGRICACPGDRKADEHYREQQALNESSAKNGASKRAFKOSPAPVAPALGA 342
 Db 294 QVLGRRCFARICACPGDRKADEHSIRKQV--SDSTKNGDGTGRFRONTGHIQ--T 349
 QY 343 GVKRRHGDDEYYIYQVGRNFEILMKLESLELMELVPQPLVDSYRQOQO-----LLQ 397
 Db 350 SIKKRSPPDELLYLPVGRRETYEMLLIKESLELMOYLPOHTIETYRQOQOQHLLQ 409
 QY 398 RPSHLQ-PPSYGVLSPMNKYGKGNKLPVSNQVLVGQPPHSSAATPNLGPVPG-----M 452
 Db 410 KQTSIQSPSSGSPPLNKNM-SMNKLPVSQLIN--PQORNALPTTTPDGMGANITPM 466
 QY 453 LNNHGHAVPANGEMSSSSAQSWSGSHCTPPPHADPSVSLTGLGCPNCI 506

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Db 467 MGTH---MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPTDCSIVSFLARLGCSSCL 523
QY 507 EYFTSQGLSIYHLQNLIEDLGALKIPEQYRMTIWRGLQDLKQGHYDSTAQOLLRS-SN 565
Db 524 DFTTQGLTIYQIEHYSDMLASLUKIQEQRHAIWKIILDHQKLFHFFSPSHLLRTPSS 583
QY 566 AATISIGSGELQORVMEAVHFRVHTITIPNRGGPGGPGGWDGFDLPCKARKQP 625
Db 584 ASTVSV-GSSETRGERVIDAVRFTLRQITSPFPR-----DEWDFNEDMDARRNKQOR 635
QY 626 IKKE 629
Db 636 IKKE 639

RESULT 7
Q9H3D4 ID Q9H3D4 PRELIMINARY; PRT; 680 AA.
AC Q9H3D4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TA P63 ALPHA.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKee F.,
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities."
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McKenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF124539; AAG45607.1; JOINED.
DR EMBL; AF124528; AAG45607.1; JOINED.
DR EMBL; AF124529; AAG45607.1; JOINED.
DR EMBL; AF124531; AAG45607.1; JOINED.
DR EMBL; AF124532; AAG45607.1; JOINED.
DR EMBL; AF124533; AAG45607.1; JOINED.
DR EMBL; AF124534; AAG45607.1; JOINED.
DR EMBL; AF124535; AAG45607.1; JOINED.
DR EMBL; AF124536; AAG45607.1; JOINED.
DR EMBL; AF124537; AAG45607.1; JOINED.
DR EMBL; AF124538; AAG45607.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN.1.
SQ SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;

Query Match 52.9%; Score 1790; DB 4; Length 680;
Best Local Similarity 55.1%; Pred. No. 1.2e-139;
Matches 366; Conservative 94; Mismatches 144; Indels 60; Gaps 18;

QY 1 MAQSTAT-----SPDGGTTFEHLWSSLEP-----DSYFDLPQSSRGNEWVGTDSS 48
Db 40 MSQQTQNEFLSPE---VFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKI----EIS 92
QY 49 MDVTHLGMTS-----VMAQFNLLSTMDQSSRAASAPYTPPEHAA-SVPTHSPTAQP 102
Db 93 MDCIRMODSLSDPMPWQYNTNLGLNMDQIQONGSSSTSPYNTDHAQNSVTPSPYAQP 152

103 STFTDMSAPVIPSNTDYPGPHFEVTFQSSSTAKSATWTYSPLLKLYCQIAKTCPIQ 162
153 STFDALSSPAIPSTNDYPGPHSDVFSFQSSSTAKSATWTYSPLLKLYCQIAKTCPIQ 212
QY 163 IKYSTPPPGTAIRAMPYKKAHVTDVVKPCPNHGLGRDFNFGOSAPASHLIRVGNL 222
Db 213 IKYMTPPPGAVIRAMPYKKAHVTEVVKPCPNHGLSRFNEQIAPPSHLIRVGNH 272
QY 223 SOYVDDPVATGROSVVVPEPQVGFETTLINFCMNCSSCVGGNNRRLIITLEMRDG 282
Db 273 AQVIEDPIITGRQSLVPEPQVGFETTLINFCMNCSSCVGGNNRRLIITLETRDG 332
QY 283 QVLGRSPFGRICACPGDRDKADEHYREOQALNESSAKNGAKRAFKQSPVAPALGA 342
Db 333 QVLGRRCFEARICACPGDRDKADESIRKQV--SDSTKNGDGTGRFRFNTHTGIM--T 388
QY 343 GVKRRHGDDETYILQVRGRENFEILMKLESLELMELVPOPLVDYSYRQOQ-----LIQ 397
Db 389 SIKKRSPPDELLYLPVGRRETYEMLLAIKESLELMQYLPQHTTETVROQQOQHQLLQ 448
QY 398 RPSHLQ-PPSYGPVLSPMKNVHGKMLPSVNLVQGPVPPHSSAATENLGPVGP-----M 452
Db 449 KQTSIQSPSSYGNSSPPLNKMN-SMNKLPVSQLIN--POQRNALTTFTIPDGMGANIPM 505
QY 453 LNNHGHAVPANGEMSSSSSAQ-----SMVSGSHCTPPPYHADPSVLSVLTGLGCPNCI 506
Db 506 MGTH---MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPTDCSIVSFLARLGCSSCL 562
QY 507 EYFTSQGLSIYHLQNLIEDLGALKIPEQYRMTIWRGLQDLKQGHYDSTAQOLLRS-SN 565
Db 563 DFTTQGLTIYQIEHYSDMLASLUKIQEQRHAIWKIILDHQKLFHFFSPSHLLRTPSS 622
QY 566 AATISIGSGELQORVMEAVHFRVHTITIPNRGGPGGPGGWDGFDLPCKARKQP 625
Db 623 ASTVSV-GSSETRGERVIDAVRFTLRQITSPFPR-----DEWDFNEDMDARRNKQOR 674
QY 626 IKKE 629
Db 675 IKKE 678

RESULT 8
Q99JE3 ID Q99JE3 PRELIMINARY; PRT; 663 AA.
AC Q99JE3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TA1 KET ALPHA PROTEIN.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-TONGUE;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants."
RL FEBS Lett. 501:121-126(2001).
DR EMBL; AJ277446; CAC37098.1;
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN.1.
SQ SEQUENCE 663 AA; 74660 MW; C953BBAC389D5B70 CRC64;

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Query Match          52.9%; Score 1789; DB 11; Length 663;
Best Local Similarity 55.1%; Pred. No. 1.4e-139;
Matches 366; Conservative 93; Mismatches 145; Indels 60; Gaps 18;

QY 1 MAQSTAT-----SPDGGTTFEHLWSLEP-----DSTYFDLPQSSRGNEVVGTDSS 48
DB 23 MSOSTOTSEFLSPE---VFQHWDFLEQPCISVQPIELNFVDEPSENGATNKI----EIS 75
QY 49 MDVHELEGMTTS-----VMAQFNLLSSTMDQMSRAASAPYTPPEHAA-SVTPHSPYAP 102
DB 76 MDCIRMQSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTPAPSYAP 135
QY 103 STFTDMSPPAPYIPNTDYPGPHFEVTFQOSSTAKSATWTYSPLKLYCQIAKTCPIQ 162
DB 136 STFDALSPSPAIPNTDYPGPHFEVTFQOSSTAKSATWTYSPLKLYCQIAKTCPIQ 195
QY 163 IKVSTPPPGTAIRAMPYVYKAEHVTVKRCPNHLEGRDNFEGQAPASHLIRVEGNL 222
DB 196 IKVSTPPPGTAIRAMPYVYKAEHVTVKRCPNHLEGRDNFEGQAPASHLIRVEGNL 255
QY 223-SQVDDPVTGROSVVVPEPQVGTFTTILYNPNCSSCVGGMNRRPILITILEMRDG 282
DB 256 AQVEDPITGROSLVLPVEPQVGTFTTILYNPNCSSCVGGMNRRPILITILEMRDG 315
QY 283 QVLRGRFEGRICACPGDRKADDEHYREQALNESAASAKRAKQSPVAPALGA 342
DB 316 QVLRGRFEGRICACPGDRKADDEHYREQALNESAASAKRAKQSPVAPALGA 371
QY 343 GVKRRHGDEYIYQVGRNFEFLMKLESLELMELVQPLVDVSYRQOOQ-----LIQ 397
DB 372 SIKRRSPDDELLYPVGRRETYEMLKIKESLELMELVQPLVDVSYRQOOQOOHLLQ 431
QY 398 RPSHLQ-PPSYGVLSPMKNVHGKMLPSVNLVGGPPPHSSAATPNLGPVGP-----M 452
DB 432 KOTSMQSSQSYGNSSPPLNKN-SMNLKPSVSLIN--POORNALPTTMTPEGMGANIPM 488
QY 453 LNNHGHAVPANGEMSSSSHAQ-----SMVSGSHCTPPPPYHADPSLVFLTGLGCPNCI 506
DB 489 MGTHT---MPMAGDMGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCL 545
QY 507 EYFTSOGLOSIVHLQNLITIEDLGALKIPEQYRMTIWRGLQDLQGHDYSTAQOLLS-SN 565
DB 546 DYFTTQGLTIIYQIHYSMDDLASLKIPEQYRMTIWRGLQDLQGHDYSTAQOLLS-SN 605
QY 566 AATISIGSGELQORVMEVHFVRHTITIPNRRGGGGGDEWADFGDLPCKARKOP 625
DB 606 ASIVSV-GSSETRGERVIDAVRFTLRQITISFPFR-----DEWDFNFDMSRRNKQOR 657
QY 626 IKEE 629
DB 658 IKEE 661

RESULT 9
O88898 PRELIMINARY; PRT; 680 AA.
AC O88898;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE TA*P63 ALPHA.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kagan M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities."
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RL Mol. Cell 2:305-316(1998).
DR EMBL; AF075436; AAC62641.1; -.
DR HSSP; P04637; 1YCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
SQ SEQUENCE 680 AA; 76788 MW; 8DF0284F247C68A CRC64;

Query Match          52.9%; Score 1789; DB 11; Length 680;
Best Local Similarity 55.1%; Pred. No. 1.4e-139;
Matches 366; Conservative 94; Mismatches 144; Indels 60; Gaps 18;

QY 1 MAQSTAT-----SPDGGTTFEHLWSLEP-----DSTYFDLPQSSRGNEVVGTDSS 48
DB 40 MSOSTOTSEFLSPE---VFQHWDFLEQPCISVQPIELNFVDEPSENGATNKI----EIS 92
QY 49 MDVHELEGMTTS-----VMAQFNLLSSTMDQMSRAASAPYTPPEHAA-SVTPHSPYAP 102
DB 93 MDCIRMQSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTPAPSYAP 152
QY 103 STFTDMSPPAPYIPNTDYPGPHFEVTFQOSSTAKSATWTYSPLKLYCQIAKTCPIQ 162
DB 153 STFDALSPSPAIPNTDYPGPHFEVTFQOSSTAKSATWTYSPLKLYCQIAKTCPIQ 212
QY 163 IKVSTPPPGTAIRAMPYVYKAEHVTVKRCPNHLEGRDNFEGQAPASHLIRVEGNL 222
DB 213 IKVSTPPPGTAIRAMPYVYKAEHVTVKRCPNHLEGRDNFEGQAPASHLIRVEGNL 272
QY 223-SQVDDPVTGROSVVVPEPQVGTFTTILYNPNCSSCVGGMNRRPILITILEMRDG 282
DB 273 AQVEDPITGROSLVLPVEPQVGTFTTILYNPNCSSCVGGMNRRPILITILEMRDG 332
QY 283 QVLRGRFEGRICACPGDRKADDEHYREQALNESAASAKRAKQSPVAPALGA 342
DB 333 QVLRGRFEGRICACPGDRKADDEHYREQALNESAASAKRAKQSPVAPALGA 388
QY 343 GVKRRHGDEYIYQVGRNFEFLMKLESLELMELVQPLVDVSYRQOOQ-----LIQ 397
DB 389 SIKRRSPDDELLYPVGRRETYEMLKIKESLELMELVQPLVDVSYRQOOQOOHLLQ 448
QY 398 RPSHLQ-PPSYGVLSPMKNVHGKMLPSVNLVGGPPPHSSAATPNLGPVGP-----M 452
DB 449 KOTSMQSSQSYGNSSPPLNKN-SMNLKPSVSLIN--POORNALPTTMTPEGMGANIPM 505
QY 453 LNNHGHAVPANGEMSSSSHAQ-----SMVSGSHCTPPPPYHADPSLVFLTGLGCPNCI 506
DB 506 MGTHT---MPMAGDMGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCL 562
QY 507 EYFTSOGLOSIVHLQNLITIEDLGALKIPEQYRMTIWRGLQDLQGHDYSTAQOLLS-SN 565
DB 563 DYFTTQGLTIIYQIHYSMDDLASLKIPEQYRMTIWRGLQDLQGHDYSTAQOLLS-SN 622
QY 566 AATISIGSGELQORVMEVHFVRHTITIPNRRGGGGGDEWADFGDLPCKARKOP 625
DB 623 ASIVSV-GSSETRGERVIDAVRFTLRQITISFPFR-----DEWDFNFDMSRRNKQOR 674
QY 626 IKEE 629
DB 675 IKEE 678

RESULT 10
O88898 PRELIMINARY; PRT; 680 AA.
ID O88898;
AC O88898;
DT 01-NOV-2000 (TRENBLrel. 15, Created)
DT 01-NOV-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE TA2 KET ALPHA.
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Db 114 SFTDALSPSPALPSNTDYPGPHSFDFVFSQOSTAKSATWYSTELKKLYCOIAKTCPIQ 173
QY 163 IKVSTPPPGPAIRAMPVYKAEHVTDVRCNPNHGLRDFNFGOSAPASHLIRVEGNL 222
Db 174 IKVSTPPPGPAIRAMPVYKAEHVTDVRCNPNHGLRDFNFGOSAPASHLIRVEGNL 233
QY 223 SOYVDDPVTGRQSVVYPPYPPQVGTETTYLYNFMCSNCSVGMNRRPILIIITLEMEDG 282
Db 234 AQYVEDPITGRQSVLVYPPYPPQVGTETTYLYNFMCSNCSVGMNRRPILIIITLEMEDG 293
QY 293 QVLRGRSEGRICACPGDRKADKEDHYREOQALNESAANKRAKQSPAPVAPALGA 342
Db 294 QVLRGRSEGRICACPGDRKADKEDHYREOQALNESAANKRAKQSPAPVAPALGA 349
QY 343 GYKRRHGDDETYLYOVRGRENFEILMKLESLELMELVPOPLVDSYRQOQO-----LLQ 397
Db 350 SIKKRSPPDELLLPVGRRETYEMLLKIKESLELMELVPOPLVDSYRQOQO-----LLQ 409
QY 398 RPSHLQ-PPSYGVLSPMKNVHGMMKLPVNLQVQPPPHSSAATPNLGPVGP-----M 452
Db 410 KQTSIQSPSSYGNSSPPLNKN-SMKNLPSVQLIN--PQORNALTPPTIPDGMGANIPM 466
QY 453 LNNHGHAVPANGEMSSSHSAQ-----SMVSGSHCTPPPPYHADPSLYSFLTGLCPNCI 506
Db 467 MGTH---NPMAGDMNGLSPQALPPPLSMPTSHCTPPPPYHADPSLYSFLTGLCPNCI 523
QY 507 EYFTSQGLQSIYHLQNTIEDLGALEIPEQYRMTIWRGLQDLKQGHYDSTAQQLRS-SN 565
Db 524 DYFTQGLTITTYQIYEHYSMDLASLKIPEQFRHAIWKILDRHQLHEFSSPHLLRTFSS 583
QY 566 AATISIGSGELQRYVMEVHFVRHTITIPNRGPGGPGDEWADFGLDPCDKARKQP 625
Db 584 ASTVSV-GSSETRGVIDAVRFLRTQTSIFPPR-----DEWDFNDFMDARANKQOR 635
QY 626 IKKE 629
Db 636 IKKE 639

RESULT 12
Q9UE10 PRELIMINARY; PRT; 680 AA.
AC Q9UE10;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE KET PROTEIN.
GN KET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE-SKELETAL MUSCLE AND KERATINOCYTE CULTURE;
RX MEDLINE=90018225; PubMed=979841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT Cloning and chromosomal mapping of the human p53-related KET gene to
RL chromosome 3q27 and its murine homolog ket to mouse chromosome 16.;
RL Mamm. Genome 9:899-902(1998).
DR EMBL; Y16961; CAA76562.1;
DR HSSP; P04637; LYCS
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

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Query Match 52.7%; Score 1782; DB 4; Length 680;
 Best Local Similarity 55.0%; Pred. No. 5.3e-139;
 Matches 365; Conservative 94; Mismatches 145; Indels 60; Gaps 18;

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QY 1 MAQSTAT-----SPDGGTTFEHLMSLEP-----DSTYFDLPSSRGNNNEVVGTDSS 48
Db 40 MSQSTQTNFLSPE---VFQIHWDFLEQPCISQVQIDLNFVDEPSEDGATNKI-----EIS 92
QY 49 MDVFLLEGMTTS-----VMAQFNLLSTMDQSSRAASASPYTPPEHAA-SYVTHSPYAPQ 102
Db 93 MDCIRKQSDLSDPWQPYNTNLGLNMQOIQNGSSSTPYTHAQNSVTAPSPYAPQ 152
QY 103 SFTFMTSPAPVPSNTDYPGPHFEVTFQOSTAKSATWYSTELKKLYCOIAKTCPIQ 162
Db 153 SFTFMTSPAPVPSNTDYPGPHFEVTFQOSTAKSATWYSTELKKLYCOIAKTCPIQ 212
QY 163 IKVSTPPPGPAIRAMPVYKAEHVTDVRCNPNHGLRDFNFGOSAPASHLIRVEGNL 222
Db 213 IKVSTPPPGPAIRAMPVYKAEHVTDVRCNPNHGLRDFNFGOSAPASHLIRVEGNL 272
QY 223 SOYVDDPVTGRQSVVYPPYPPQVGTETTYLYNFMCSNCSVGMNRRPILIIITLEMEDG 282
Db 273 AQYVEDPITGRQSVLVYPPYPPQVGTETTYLYNFMCSNCSVGMNRRPILIIITLEMEDG 332
QY 283 QVLRGRSEGRICACPGDRKADKEDHYREOQALNESAANKRAKQSPAPVAPALGA 342
Db 333 QVLRGRSEGRICACPGDRKADKEDHYREOQALNESAANKRAKQSPAPVAPALGA 388
QY 343 GYKRRHGDDETYLYOVRGRENFEILMKLESLELMELVPOPLVDSYRQOQO-----LLQ 397
Db 389 SIKKRSPPDELLLPVGRRETYEMLLKIKESLELMELVPOPLVDSYRQOQO-----LLQ 448
QY 398 RPSHLQ-PPSYGVLSPMKNVHGMMKLPVNLQVQPPPHSSAATPNLGPVGP-----M 452
Db 449 KQTSIQSPSSYGNSSPPLNKN-SMKNLPSVQLIN--PQORNALTPPTIPDGMGANIPM 505
QY 453 LNNHGHAVPANGEMSSSHSAQ-----SMVSGSHCTPPPPYHADPSLYSFLTGLCPNCI 506
Db 506 MGTH---NPMAGDMNGLSPQALPPPLSMPTSHCTPPPPYHADPSLYSFLTGLCPNCI 562
QY 507 EYFTSQGLQSIYHLQNTIEDLGALEIPEQYRMTIWRGLQDLKQGHYDSTAQQLRS-SN 565
Db 563 DYFTQGLTITTYQIYEHYSMDLASLKIPEQFRHAIWKILDRHQLHEFSSPHLLRTFSS 622
QY 566 AATISIGSGELQRYVMEVHFVRHTITIPNRGPGGPGDEWADFGLDPCDKARKQP 625
Db 623 ASTVSV-GSSETRGVIDAVRFLRTQTSIFPPR-----DEWDFNDFMDARANKQOR 674
QY 626 IKKE 629
Db 675 IKKE 678

RESULT 13
O89097 PRELIMINARY; PRT; 586 AA.
AC O89097;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE DN P63 ALPHA.
DE DN P63 ALPHA.
GN TRP63 OR P73H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kachhad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.;
RA Caput D., McKean F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE-THYMUS;
RX MEDLINE=98369596; PubMed=9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
RT Tanaka T., Shinkai Y., Kato H.;
RL "A second p53-related protein, p73L, with high homology to p73.";
RL Biochem. Biophys. Res. Commun. 248:603-607(1998).
DR EMBL; AF075439; AAC62844.1; -
DR EMBL; AB010152; BAA32432.1; -
DR HSSP; P04637; LYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53_1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
SQ SEQUENCE 586 AA; 65789 MW; 622E240858BDBC7 CRC64;

Query Match 51.5%; Score 1743; DB 11; Length 586;
Best Local Similarity 59.7%; Pred. No. 7 3e-136;
Matches 347; Conservative 82; Mismatches 116; Indels 36; Gaps 13;

QY 67 LLSTMDQMSRAASASPTPEHAA-SVPTHSPYAQPSSTFDMSAPVPSNTDYPGPH 125
Db 22 LLNSMDQQIQNGSSSTSYNDHAQNSVTAPSPYAQPSSTFDALSPSPAIPNTDYPGPH 81
QY 126 HEVTFQOSTAKSATWTYSPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKAE 185
Db 82 SEDVSFQOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPGAVIRAMPVYKAE 141
QY 186 HVTDVVKRCNPHELGRDFNEGQSPASHLRVEGNLSQYDDPVTCGROSVVPEPQV 245
Db 142 HVTDVVKRCNPHELGRDFNEGQSPASHLRVEGNLSQYDDPVTCGROSVVPEPQV 201
QY 246 GTEFTTILYNFMCNNSCVGGNRRPILIIITLEMRDQVLRGRSFEGRCACPGDRKAD 305
Db 202 GTEFTTILYNFMCNNSCVGGNRRPILIIITLETRDQVLRGRSFEGRCACPGDRKAD 261
QY 306 EDHYREQQALNESSAKNGAASKRAFQSPAPVAGALGAGVKKRRHGEDTYIYLVQVGRNF 365
Db 262 EDSIRKQV--SDSAKNGDGTFRPQNTGHIQ--TSIKKRSPPDELLYLVRGRETY 317
QY 366 EILMKIKESLELMELVPPQPLVDSYRQOQ-----LLQRPShLQ-PPSYGVLSPNKKVHG 419
Db 318 EMLKIKESLELMELVPPQPLVDSYRQOQ-----LLQRPShLQ-PPSYGVLSPNKKVHG 376
QY 420 GNNKLPVNLQVGPQPPHSSAATPNLGPVGP-----MLNNHGAHPANGEMSSSSHAQ-- 473
Db 377 SNMKLPVNLQVGPQPPHSSAATPNLGPVGP-----MLNNHGAHPANGEMSSSSHAQ-- 431
QY 474 ----SWSGSHTPPPHADPSLVFLTGLGCPNCIEYTSOGLOSTIHLQNTIEDIG 529
Db 432 PPLSPMSTSHCTPPPPYPTDCISVFLARLGCSCLDYFTTQGLTIIQIHYSDMLIA 491
QY 530 ALKIQEQRWMTWRGLDLKQGHYDYTAQQLRS--SNAATISIGSGELQRQRVMEAVHF 588
Db 492 SLKIQEQRHAIWKILDRHLDFSSPHLLRTPSGASVSV--GSSETRGERVIDAVRF 550
QY 589 RVNHTITIPNRGGGGGDEWADFGLDPCCKARKPIKEE 629
Db 551 TLRQITSEPPR-----DEWDFNDFDMSRRNKQRIKEE 584

RESULT 14
Q9UBV9 PRELIMINARY; PRT; 586 AA.
AC Q9UBV9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE DE P53 ALPHA.
GN P53.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1] NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Raghav M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RX SEQUENCE FROM N.A.
RX Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
RA Dellavalle R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,
RA Jablonska S.;
RT "Characterization of an autoantigen associated with chronic ulcerative
RT stomatitis: The CUSP autoantigen is a member of the p53 family.";
RL J. Invest. Dermatol. 0:0-0(1999).
RN [3]
RX SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075431; AAC62636.1; -
DR EMBL; AF091627; AAC43038.1; -
DR EMBL; AF124539; AAG45610.1; -
DR EMBL; AF124530; AAG45610.1; JOINED.
DR EMBL; AF124531; AAG45610.1; JOINED.
DR EMBL; AF124532; AAG45610.1; JOINED.
DR EMBL; AF124533; AAG45610.1; JOINED.
DR EMBL; AF124534; AAG45610.1; JOINED.
DR EMBL; AF124535; AAG45610.1; JOINED.
DR EMBL; AF124537; AAG45610.1; JOINED.
DR EMBL; AF124538; AAG45610.1; JOINED.
DR HSSP; P04637; LYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
SQ SEQUENCE 586 AA; 65756 MW; 2E292ABF1AF8629 CRC64;

Query Match 51.4%; Score 1741; DB 4; Length 586;
Best Local Similarity 59.6%; Pred. No. 1 1e-135;
Matches 346; Conservative 84; Mismatches 115; Indels 36; Gaps 13;

QY 67 LLSTMDQMSRAASASPTPEHAA-SVPTHSPYAQPSSTFDMSAPVPSNTDYPGPH 125
Db 22 LLNSMDQQIQNGSSSTSYNDHAQNSVTAPSPYAQPSSTFDALSPSPAIPNTDYPGPH 81
QY 126 HEVTFQOSTAKSATWTYSPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKAE 185
Db 82 SEDVSFQOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPGAVIRAMPVYKAE 141
QY 186 HVTDVVKRCNPHELGRDFNEGQSPASHLRVEGNLSQYDDPVTCGROSVVPEPQV 245
Db 142 HVTDVVKRCNPHELGRDFNEGQSPASHLRVEGNLSQYDDPVTCGROSVVPEPQV 201
QY 246 GTEFTTILYNFMCNNSCVGGNRRPILIIITLEMRDQVLRGRSFEGRCACPGDRKAD 305
Db 202 GTEFTTILYNFMCNNSCVGGNRRPILIIITLETRDQVLRGRSFEGRCACPGDRKAD 261
QY 306 EDHYREQQALNESSAKNGAASKRAFQSPAPVAGALGAGVKKRRHGEDTYIYLVQVGRNF 365
Db 262 EDSIRKQV--SDSAKNGDGTFRPQNTGHIQ--TSIKKRSPPDELLYLVRGRETY 317
QY 366 EILMKIKESLELMELVPPQPLVDSYRQOQ-----LLQRPShLQ-PPSYGVLSPNKKVHG 419
Db 318 EMLKIKESLELMELVPPQPLVDSYRQOQ-----LLQRPShLQ-PPSYGVLSPNKKVHG 376
QY 420 GNNKLPVNLQVGPQPPHSSAATPNLGPVGP-----MLNNHGAHPANGEMSSSSHAQ-- 473

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Db 377 SNKLPVSQLIN--PQORNALPTTIPDGMGANIPMGTH---MPMAGDMNGLSPTQAL 431
Qy 474 ----SMVSGSHCTPPPPYHADPSLVSLFGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLG 529
Db 432 PPPLSMFSTSHCTPPPPYHADPSLVSLFGLGCPNCEIYFTSQGLQSIYHLQNLTIEDLG 491
Qy 530 ALKIPQYRMTIWRGLQDLKQGHDSYTAQOLLRS--SNAATISIGSGELQORVMEAVHF 588
Db 492 SLKIPQYRMTIWRGLQDLKQGHDSYTAQOLLRS--SNAATISIGSGELQORVMEAVHF 550
Qy 589 RVRHTTIPNRGSGGGPDDEWADFGLPDCRKARQPIKEE 629
Db 551 TLQRTISFPFR-----DEWDFNDFMDARRNKQRIKEE 584

RESULT 15
Q99JE2 PRELIMINARY; PRT; 586 AA.
AC Q99JE2;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE DN KET ALPHA PROTEIN.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H1STAR; TISSUE=TONGUE;
EX MEDLINE=2163378; PubMed=11470269;
RA Bamberger C.; Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants."
RL FEBS Lett. 501:121-126(2001).
DR EMBL; AJ277447; CAC37099.1; -
DR HSP; P04637; LYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001680; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; P00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 586 AA; 65732 MW; 78AB8CC4F52BA743; CRC64;

Query Match 51.4%; Score 1740; DB 11; Length 586;
Best Local Similarity 58.1%; Pred. NO. 1.3e-135;
Matches 348; Conservative 86; Mismatches 121; Indels 44; Gaps 14;

Qy 57 MTSVMAQFN-----LLSTMDQMSRAASAPYTPHAA-SVPTHSPYAPQPSSTFD 107
Db 4 LESNAQTFSEPOYTNLGLNGMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPQPSSTFD 63
Qy 108 TMSAPVIPSNTDYPGPHFVTFQOSSTAKSATWTYSPLKLYCQIAKTCPIQIKVST 167
Db 64 ALSPSAIPSTNDYPGPHFVTFQOSSTAKSATWTYSPLKLYCQIAKTCPIQIKVMT 123
Qy 168 PPPPGTAIRAMPYKKAHVTDVVKRCPNHELGRDFNEGOSAPASHLRVVEGNLSQYVD 227
Db 124 PPQGAIVRAMPYKKAHVTEVVKRCPNHELGRDFNEGOSAPASHLRVVEGNLSQYVD 183
Qy 228 DPTVGQSVVVPYEPQVQTEFTTILYNFMCNCSVCGGNRRPILIIITLMDRGQVLGR 287
Db 184 DPTVGQSVLVYEPQVQTEFTTILYNFMCNCSVCGGNRRPILIIITLMDRGQVLGR 243
Qy 288 RSEGRICACPGDRKADHDYREQQALNESSAKNGAKAFKQSPVAPALGAGVKR 347
Db 244 RCFEARIACPGDRKADHDYREQQALNESSAKNGAKAFKQSPVAPALGAGVKR 299
Qy 348 RHGEDTYTLQVRGRENFFELMKLESLELMELVPLQPLVDYSYRQOQ-----LLQRPShL 402
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Db 300 RSPDELLYLPVRGRETIEYEMLLAKESLELMQYLPQHTIETVYRQOQOQHOLQKOTSM 359
Qy 403 Q-PPSYGVLSPMKNVHGNNKLPVSNQLVGPPPHSSAATPNLGPVCPG----MLNHHG 457
Db 360 QSQSSYGNSSPPLNKN-SNKLPSVSQLIN--PQORNALPTTIPMPEGGANIPMGTH- 415
Qy 458 HAVPANGEMSSSSHAQ-----SMVSGSHCTPPPPYHADPSLVSLFGLGCPNCEIYFTS 511
Db 416 --MPMAGDMNGLSPTQALPPPLSMFSTSHCTPPPPYHADPSLVSLFGLGCPNCEIYFTS 473
Qy 512 QGLQSIYHLQNLTIEDLGALKIPQYRMTIWRGLQDLKQGHDSYTAQOLLRS--SNAATIS 570
Db 474 QGLTIIQIEHYSMDDLAKLIPQYRMTIWRGLQDLKQGHDSYTAQOLLRS--SNAATIS 533
Qy 571 IGGSGELQORVMEAVHFRVHTTIPNRGSGGGPDDEWADFGLPDCRKARQPIKEE 629
Db 534 V-GSSETRGERVIDAVRFTLQRTISFPFR-----DEWDFNDFMDARRNKQRIKEE 584
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